

SEQUENCE LISTING

<110> WOLD, WILLIAM
TOLLEFSON, ANN

<120> ADENOVIRUS REPLICATION-COMPETENT VECTORS EXPRESSING
TRAIL

<130> INGN:106US

<140> UNKNOWN

<141> 2004-03-26

<150> 60/458,493

<151> 2003-03-28

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1769

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (88)..(933)

<400> 1

cctcactgac tataaaagaa tagagaagga agggcttcag tgaccggctg cctggctgac 60

ttacagcagt cagactctga caggatc atg gct atg atg gag gtc cag ggg gga 114
Met Ala Met Met Glu Val Gln Gly Gly

1

5

ccc agc ctg gga cag acc tgc gtg ctg atc gtg atc ttc aca gtg ctc 162
Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu
10 15 20 25

ctg cag tct ctc tgt gtg gct gta act tac gtg tac ttt acc aac gag 210
Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu
30 35 40

ctg aag cag atg cag gac aag tac tcc aaa agt ggc att gct tgt ttc 258
Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe
45 50 55

tta aaa gaa gat gac agt tat tgg gac ccc aat gac gaa gag agt atg 306
Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met
60 65 70

aac agc ccc tgc tgg caa gtc aag tgg caa ctc cgt cag ctc gtt aga 354
Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg
75 80 85

aag atg att ttg aga acc tct gag gaa acc att tct aca gtt caa gaa 402

Lys	Met	Ile	Leu	Arg	Thr	Ser	Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu		
90					95					100					105		
aag	caa	caa	aat	att	tct	ccc	cta	gtg	aga	gaa	aga	ggg	cct	cag	aga	450	
Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg		
			110					115					120				
gta	gca	gct	cac	ata	act	ggg	acc	aga	gga	aga	agc	aac	aca	ttg	tct	498	
Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser		
			125					130					135				
tct	cca	aac	tcc	aag	aat	gaa	aag	gct	ctg	ggc	cgc	aaa	ata	aac	tcc	546	
Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser		
		140					145					150					
tgg	gaa	tca	tca	agg	agt	ggg	cat	tca	ttc	ctg	agc	aac	ttg	cac	ttg	594	
Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu		
	155					160					165						
agg	aat	ggg	gaa	ctg	gtc	atc	cat	gaa	aaa	ggg	ttt	tac	tac	atc	tat	642	
Arg	Asn	Gly	Glu	Leu	Val	Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr		
170					175				180					185			
tcc	caa	aca	tac	ttt	cga	ttt	cag	gag	gaa	ata	aaa	gaa	aac	aca	aag	690	
Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys		
			190						195					200			
aac	gac	aaa	caa	atg	gtc	caa	tat	att	tac	aaa	tac	aca	agt	tat	cct	738	
Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro		
		205					210						215				
gac	cct	ata	ttg	ttg	atg	aaa	agt	gct	aga	aat	agt	tgt	tgg	tct	aaa	786	
Asp	Pro	Ile	Leu	Leu	Met	Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys		
		220				225						230					
gat	gca	gaa	tat	gga	ctc	tat	tcc	atc	tat	caa	ggg	gga	ata	ttt	gag	834	
Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu		
	235				240						245						
ctt	aag	gaa	aat	gac	aga	att	ttt	gtt	tct	gta	aca	aat	gag	cac	ttg	882	
Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu		
250					255					260				265			
ata	gac	atg	gac	cat	gaa	gcc	agt	ttt	ttc	ggg	gcc	ttt	tta	gtt	ggc	930	
Ile	Asp	Met	Asp	His	Glu	Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly		
			270					275					280				
taa	ctgac	ctgga	aagaaaa	agc	aataac	ctca	aagt	gactat	tcag	ttttca						983	
ggatgataca	ctatga	agat	gtttcaaaaa	atctgac	caa	aacaa	caaaa	cagaaa	acag							1043	
aaaacaaaaa	aacct	tctatg	caatctg	agt	agagc	agcca	caac	caaaaa	attct	taca	ac					1103	
acacactgtt	ctgaa	agtga	ctcact	tatc	ccaag	aaaat	gaaatt	gctg	aaagat	cttt						1163	
caggactcta	cctcat	atca	gtttg	ctagc	agaaat	ctag	aagact	gtca	gctt	ccaa	ac					1223	

attaatgcaa tgggtaacat cttctgtctt tataatctac tccttgtaaa gactgtagaa 1283
 gaaagcgcaa caatccatct ctcaagtagt gtatcacagt agtagcctcc aggtttcctt 1343
 aagggacaac atccttaagt caaaagagag aagaggcacc actaaaagat cgcagtttgc 1403
 ctggtgcagt gggtcacacc tgtaatccca acattttggg aaccaaggt gggtagatca 1463
 cgagatcaag agatcaagac catagtgacc aacatagtga aaccccatct ctactgaaag 1523
 tgcaaaaatt agctgggtgt gttggcacat gcctgtagtc ccagctactt gagaggctga 1583
 ggcaggagaa tcgtttgaac ccgggaggca gaggttgtag tgtggtgaga tcatgccact 1643
 acactccagc ctggcgacag agcgagactt ggtttcaaaa aaaaaaaaaa aaaaaaactt 1703
 cagtaagtac gtgttatttt tttcaataaa attctattac agtatgtcaa aaaaaaaaaa 1763
 aaaaaa 1769

<210> 2
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
 1 5 10 15
 Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
 20 25 30
 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
 35 40 45
 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
 50 55 60
 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
 65 70 75 80
 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
 85 90 95
 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
 100 105 110
 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
 115 120 125
 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
 130 135 140
 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
 145 150 155 160
 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
 165 170 175
 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
 180 185 190
 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
 195 200 205
 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
 210 215 220
 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr

225								230								235				240
Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile					
				245						250						255				
Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala					
				260						265						270				
Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly												
				275						280										